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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/645,415A

DATE: 01/29/2002
TIME: 14:21:10

Input Set : A:\8002059999.app
Output Set: N:\CRF3\01292002\I645415A.raw

P.S.

4 <110> APPLICANT: Bermudes, G.
 5 King, I.
 6 Clairmont, C.
 7 Lin, S.
 8 Belcourt, M.
 10 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 11 TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
 14 <130> FILE REFERENCE: 8002-059
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/645,415A
 C--> 16 <141> CURRENT FILING DATE: 2000-08-24
 16 <150> PRIOR APPLICATION NUMBER: 60/157,581
 17 <151> PRIOR FILING DATE: 1999-10-04
 19 <150> PRIOR APPLICATION NUMBER: 60/157,637
 20 <151> PRIOR FILING DATE: 1999-10-04
 22 <160> NUMBER OF SEQ ID NOS: 61
 24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 26
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: Forward primer
 34 <400> SEQUENCE: 1
 35 gaagatcttc cggaggaggg gaaatg 26
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 44
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Artificial Sequence
 42 <220> FEATURE:
 43 <223> OTHER INFORMATION: Reverse primer
 45 <400> SEQUENCE: 2
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 48 <210> SEQ ID NO: 3
 49 <211> LENGTH: 477
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 51 <213> ORGANISM: Homo sapiens
 53 <220> FEATURE:
 54 <221> NAME/KEY: CDS
 55 <222> LOCATION: (1)...(474)
 57 <400> SEQUENCE: 3
 58 atg gta cgt agc tcc tct cgc act ccg tcc gat aag ccg gtt gct cat 48
 59 Met Val Arg Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 60 1 5 10 15

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62	gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt	.96
63	Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
64	20 25 30	
66	cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctc cgt gat aac cag	144
67	Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
68	35 40 45	
70	ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg	192
71	Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
72	50 55 60	
74	tcc aag ggt cag ggc tgc ccg tcg act cat gtt ctg ctg act cac acc	240
75	Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
76	65 70 75 80	
78	atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc	288
79	Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
80	85 90 95	
82	gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg	336
83	Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
84	100 105 110	
86	aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag	384
87	Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
88	115 120 125	
90	aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat	432
91	Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
92	130 135 140	
94	tcc gct gaa tct ggc cag gtc tac ttc ggt att atc gca ctg	474
95	Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu	
96	145 150 155	
98	taa	477
100	<210> SEQ ID NO: 4	
101	<211> LENGTH: 158	
102	<212> TYPE: PRT	
103	<213> ORGANISM: Homo sapiens	
105	<400> SEQUENCE: 4	
106	Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
107	1 5 10 15	
108	Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
109	20 25 30	
110	Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
111	35 40 45	
112	Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
113	50 55 60	
114	Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
115	65 70 75 80	
116	Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
117	85 90 95	
118	Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
119	100 105 110	
120	Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
121	115 120 125	

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122 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 123 130 135 140
 124 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 125 145 150 155

127 <210> SEQ ID NO: 5
 128 <211> LENGTH: 28
 129 <212> TYPE: DNA
 130 <213> ORGANISM: Artificial Sequence
 132 <220> FEATURE:
 133 <223> OTHER INFORMATION: Forward primer
 135 <400> SEQUENCE: 5
 136 ccgacgcgtt gacacctgaa aactggag 28
 138 <210> SEQ ID NO: 6
 139 <211> LENGTH: 29
 140 <212> TYPE: DNA
 141 <213> ORGANISM: Artificial Sequence
 143 <220> FEATURE:
 144 <223> OTHER INFORMATION: Reverse primer
 146 <400> SEQUENCE: 6
 147 ccgacgcgtg aaaggatctc aagaagatc 29
 149 <210> SEQ ID NO: 7
 150 <211> LENGTH: 543
 151 <212> TYPE: DNA
 152 <213> ORGANISM: Artificial Sequence
 154 <220> FEATURE:
 155 <223> OTHER INFORMATION: Fusion construct
 157 <221> NAME/KEY: CDS
 158 <222> LOCATION: (1)...(540)
 160 <400> SEQUENCE: 7
 161 atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct 48
 162 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 163 1 5 10 15
 165 acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc 96
 166 Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
 167 20 25 30
 169 gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag 144
 170 Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
 171 35 40 45
 173 ctg cag tgg ctg aac cgt cgc gct aac gcc ctg ctg gca aac ggc gtt 192
 174 Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
 175 50 55 60
 177 gag ctc cgt gat aac cag ctc gtg gta cct tct gaa ggt ctg tac ctg 240
 178 Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
 179 65 70 75 80
 181 atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tcg act cat 288
 182 Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
 183 85 90 95
 185 gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc 336
 186 Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr

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187	100	105	110	
189	aaa gtt aac ctg ctg ägc gct atc aag tct ccg tgc cag cgt gaa act			384
190	Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr			
191	115	120	125	
193	ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt			432
194	Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly			
195	130	135	140	
197	ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac			480
198	Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn			
199	145	150	155	160
201	cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt			528
202	Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly			
203	165	170	175	
205	att atc gca ctg taa			543
206	Ile Ile Ala Leu			
207	180			
210	<210> SEQ ID NO: 8			
211	<211> LENGTH: 180			
212	<212> TYPE: PRT			
213	<213> ORGANISM: Artificial Sequence			
215	<220> FEATURE:			
216	<223> OTHER INFORMATION: Fusion construct			
218	<400> SEQUENCE: 8			
219	Met Lys Lys Thr Ala Ile Ala Val Ala Leu Ala Gly Phe Ala			
220	1	5	10	15
221	Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser			
222	20	25	30	
223	Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln			
224	35	40	45	
225	Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val			
226	50	55	60	
227	Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu			
228	65	70	75	80
229	Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His			
230	85	90	95	
231	Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr			
232	100	105	110	
233	Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr			
234	115	120	125	
235	Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly			
236	130	135	140	
237	Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn			
238	145	150	155	160
239	Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly			
240	165	170	175	
241	Ile Ile Ala Leu			
242	180			
244	<210> SEQ ID NO: 9			
245	<211> LENGTH: 801			

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246 <212> TYPE: DNA
 247 <213> ORGANISM: Artificial Sequence
 249 <220> FEATURE:
 250 <223> OTHER INFORMATION: Fusion construct
 252 <221> NAME/KEY: CDS
 253 <222> LOCATION: (1)...(798)
 255 <400> SEQUENCE: 9

256 atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct	48
257 Met Lys Lys Thr Ala Ile Ala Val Ala Leu Ala Gly Phe Ala	
258 1 5 10 15	
260 acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac	96
261 Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp	
262 20 25 30	
264 aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt	144
265 Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser	
266 35 40 45	
268 tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa	192
269 Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln	
270 50 55 60	
272 gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc	240
273 Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr	
274 65 70 75 80	
276 tct gag gaa acc att tct aca gtt caa gaa aag caa aat att tct	288
277 Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser	
278 85 90 95	
280 ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act	336
281 Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr	
282 100 105 110	
284 ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat	384
285 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn	
286 115 120 125	
288 gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt	432
289 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser	
290 130 135 140	
292 ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc	480
293 Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val	
294 145 150 155 160	
296 atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga	528
297 Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg	
298 165 170 175	
300 ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc	576
301 Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val	
302 180 185 190	
304 caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg	624
305 Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met	
306 195 200 205	
308 aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc	672
309 Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu	
310 210 215 220	

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
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Input Set : A:\8002059999.app
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L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59